IN THE CLAIMS:

Applicants, pursuant to 37 C.F.R. § 1.121, submit the following amendments to the claims:

1. (Currently amended) A method for predicting the responsiveness of a subject[[s]] with a breast tissue cell proliferative disorder[[,]] to a therapy, ~~involving treatment with or more drugs that target the estrogen receptor pathway or that are involved in estrogen metabolism, production or secretion, said method~~ comprising:

obtaining, prior to or during therapeutic treatment of a subject having a breast tissue cell proliferative disorder, a biological sample comprising genomic DNA from the subject, wherein the therapeutic treatment comprises treatment with one of more drugs that target the estrogen receptor pathway or that are involved in estrogen metabolism, production or secretion; and

determining~~analysing~~ the genomic DNA methylation status of at least one CpG dinucleotide of at least one target nucleic acid[[s]] sequence of ~~selected from the gene group consisting of STMN1, SFN, S100A2, TGFBR2, TP53, PTGS2, FGFR1, SYK, PITX2, GRIN2D, PSA, CGA, CYP2D6, MSMB, COX7A2L, VTN, PRKCD, ONECUT2, WBP11, CYP2D6, DAG1, ERBB2, S100A2, TFF1, TP53, TMEFF2, ESR1, SYK, RASSF1, PITX2, PSAT1, CGA, PCAF~~the PITX2 gene, and the regulatory regions thereof by contacting the at least one target nucleic acid[[s]] sequence ~~in a biological sample, obtained from said subject prior to or during the treatment~~ with one or more agents suitable to convert cytosine bases that are unmethylated at the 5'-position thereof to a base that is detectably dissimilar to cytosine in terms of hybridisation properties, wherein predicting responsiveness of the subject to the therapy is afforded.

2.-16. (Withdrawn)

17. (Currently amended) The method of claim 1, wherein the at least one target nucleic acid sequence is selected from the group consisting of SEQ ID NO:83, ~~essentially of SEQ ID NOs: 27, 83, 90, 91, and~~ sequences complementary thereto, and contiguous portions thereof.

18. (Withdrawn)

19. (Currently amended) The method of claim 1, wherein ~~said~~ the at least one target nucleic acid sequence is selected from the group consisting of SEQ ID NO:135, ~~essentially of SEQ ID NOs: 126, 137, 129, 125, 132, 122, 123, 131, 133, 134, 127, 130, 135, 124, 128, 136, and~~ sequences complementary thereto, and contiguous portions thereof.

20. (Previously presented) The method of claim 1, wherein said cell proliferative disorder of the breast tissue is selected from the group consisting of ductal carcinoma in situ, lobular carcinoma, colloid carcinoma, tubular carcinoma, medullary carcinoma, metaplastic carcinoma, intraductal carcinoma in situ, lobular carcinoma in situ and papillary carcinoma in situ.

21. (Previously presented) The method of claim 1, wherein said subject[[s]] is~~are~~ at least one of estrogen and progesterone receptor positive.

22. (Previously presented) The method of claim 1, wherein said therapy is for the treatment of a relapse or metastatic cell proliferative disorder of the breast tissues.

23. (Previously presented) The method of claim 1, wherein said therapy is an adjuvant treatment.

24. (Previously presented) The method of claim 23, wherein said subject[[s]] did not receive a chemotherapeutic treatment.

25.-44. (Withdrawn)

45. (Currently amended) A method for predicting the responsiveness of a subject[[,]] with a breast cell proliferative disorder[[,]] to a therapy, ~~involving treatment with one or more drugs that target the estrogen receptor pathway or that are involved in estrogen metabolism, production or secretion, said method~~ comprising:

obtaining, prior to or during therapeutic treatment of a subject having a breast tissue cell proliferative disorder, a biological sample comprising genomic DNA from the subject, wherein the therapeutic treatment comprises treatment with one of more drugs that target the estrogen receptor pathway or that are involved in estrogen metabolism, production or secretion;

~~a) obtaining, from a subject, a biological sample containing genomic DNA;~~

[[b) ]]isolating the genomic DNA;

[[c) ]]contacting the isolated genomic DNA, or a portion thereof, with an agent or combination of agents suitable to convert cytosine bases that are unmethylated at the 5-position to uracil, or to another base which is dissimilar to cytosine in terms of base pairing behaviorbehaviour, to provide a pretreated DNA;

[[d) ]]amplifying at least one pretreated DNA sequence, or a portion thereof, selected from the sequence group consisting of SEQ ID NOS:411, 412, 515, 516, 685, 686, 789, 790, ~~SEQ ID NOS: 299, 300, 325, 326, 327, 328, 331, 332, 345, 346, 381, 382, 393, 394, 401, 402, 411, 412, 417, 418, 425, 426, 427, 428, 429, 430, 443, 444, 455, 456, 475, 476, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 573, 574, 599, 600, 601, 602, 605, 606, 619, 620, 655, 656, 667, 668, 675, 676, 685, 686, 691, 692, 699, 700, 701, 702, 703, 704, 717, 718, 729, 730, 749, 750, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794,~~ sequences complementary thereto, and contiguous portions thereof; and

[[e) ]]determining, based on the amplification or on analysis of the nucleic acid amplificate, the methylation status of one or more genomic CpG dincucleotide sequencesdinucleotides of the sequence group consisting of SEQ ID NO:83 and SEQ ID NO:135, wherein predicting responsiveness of the subject to the therapy is affordedwhereby responsiveness to the therapy is, at least in part predicted.

46.-56. (Withdrawn)

57. (Currently amended) The method of claim 45, wherein determining the methylation status ~~in e)~~ comprises sequencing.

58. (Currently amended) The method of claim 45, wherein amplifying ~~in d)~~ comprises using methylation-specific primers.

59. (Currently amended) The method of claim 45, wherein amplifying comprises~~further comprising in d)~~ use of at least one nucleic acid molecule or peptide nucleic acid molecule comprising in each case a contiguous sequence at least 9 nucleotides in length that is

complementary to, or hybridizes under moderately stringent or stringent conditions to a sequence selected from the group consisting of SEQ ID NOS:411, 412, 515, 516, 685, 686, 789, 790~~SEQ ID NOS: 299, 300, 325, 326, 327, 328, 331, 332, 345, 346, 381, 382, 393, 394, 401, 402, 411, 412, 417, 418, 425, 426, 427, 428, 429, 430, 443, 444, 455, 456, 475, 476, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 573, 574, 599, 600, 601, 602, 605, 606, 619, 620, 655, 656, 667, 668, 675, 676, 685, 686, 691, 692, 699, 700, 701, 702, 703, 704, 717, 718, 729, 730, 749, 750, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794~~, sequences complementary thereto, and contiguous portions thereof~~and complements thereof~~, wherein said at least one nucleic acid molecule or peptide nucleic acid molecule suppresses amplification of a nucleic acid to which it is hybridized.

60. (Withdrawn)

61. (Currently amended) The method of claim 45, wherein contacting ~~in c)~~ is with an agent, or combination of agents, comprising at least on one of bisulfite, hydrogen sulfite or disulfite.

62. (Currently amended) A method for predicting the responsiveness of a subject[[,]] with a breast cell proliferative disorder[[,]] to a therapy, ~~involving treatment with one or more drugs that target the estrogen receptor pathway or that are involved in estrogen metabolism, production or secretion, said method~~ comprising:

obtaining, prior to or during therapeutic treatment of a subject having a breast tissue cell proliferative disorder, a biological sample comprising genomic DNA from the subject, wherein the therapeutic treatment comprises treatment with one of more drugs that target the estrogen receptor pathway or that are involved in estrogen metabolism, production or secretion;

~~a) obtaining, from a subject, a biological sample containing genomic DNA;~~

[[b) ]]isolating the genomic DNA;

[[c) ]]digesting the isolated genomic DNA, or a portion thereof, comprising at least one

sequence selected from the sequence group consisting of SEQ ID NO:83, SEQ ID NO:135, sequences complementary thereto, and contiguous portions thereof~~SEQ ID NOS:27, 40, 41, 43, 50, 68, 74, 78, 83, 86, 90-92, 99, 105, 115, 121-137 and sequences complementary thereto~~, with one or more methylation-sensitive restriction enzymes; and

[[d) ]]determining the DNA fragments generated or not generated~~in c)~~, ~~whereby~~wherein predicting responsiveness of the subject to the therapy is afforded~~responsiveness to the therapy is, at least in part, predicted~~.

63.-66. (Withdrawn)

67. (Currently amended) The method of claim 62, further comprising, prior to determining the DNA fragments[[d)]], amplifying the DNA digest.

68.-76. (Withdrawn)

77. (Previously presented) The method of any one of claims 45 and 62, wherein the biological sample containing genomic DNA is obtained from a source selected from the group consisting of cells or cellular components which contain DNA, cell lines, histological slides, biopsies, tissue embedded in paraffin, breast tissues, blood, plasma, lymphatic fluid, lymphatic tissue, duct cells, ductal lavage fluid, nipple aspiration fluid, bone marrow, and combinations thereof.

78. (Previously presented) A kit, comprising a reagent having at least one of bisulfite disulfite, and hydrogen sulfite, as well as oligonucleotides and/or PNA-oligomers according to any one of claims 30 to 38.

79. (Previously presented) The kit of claim 78, further comprising standard reagents for performing a methylation assay selected from the group consisting of MS-SNuPE, MSP, MethyLight, HeavyMethyl, nucleic acid sequencing and combinations thereof.

80. (Cancelled)